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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=23; hr=13; min=45; sec=43; ms=375;]

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Reviewer Comments:

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG
RESTRICTION ENDONUCLEASE (as amended)

The first line of the above <120> response exceeds the Sequence Rules' required 72-character line (this includes white spaces). Please insert a hard return after "TYPE" on the first line, and align the second line.

(from Sequence 2)

Val	Asp	Glu	Ala	Leu	Leu	Ile	Lys	Tyr	His	Gly	Phe	Ser	Glu	Lys	Glu
				515						520					525

Val	Lys	Gln	Leu	Arg	Gly	Ile	Trp	Lys	Lys	Leu	Ser	Gln	Arg	Arg	Asn
				530						535					540

Asn Arg Thr Lys Lys
545

Please delete the excess blank lines above: only one blank line should separate each amino acid line.

<210> 38

<211> 103

<212> PRT

<213> artificial

<220>

<223> segment of protein sequence of catechol O-methyltransferase

<400> 39

Please change the above <210> response to "39." <210> 38 was already shown.

Application No: 10800946

Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-09 14:09:09.990

Finished: 2008-01-09 14:09:12.054

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 64 ms

Total Warnings: 25

Total Errors: 2

No. of SeqIDs Defined: 43

Actual SeqID Count: 43

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)

Input Set:

Output Set:

Started: 2008-01-09 14:09:09.990
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped

SEQUENCE LISTING

<110> Xu, Shuang-yong
Kobbe, Daniela
Zhu, Zhenyu
Samuelson, James

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG RESTRICTION ENDONUCLEASE
(as amended)

<130> NEB-183-CIP

<140> 10800946

<141> 2004-03-15

<150> 10/150,028

<151> 2002-05-17

<150> 09/693,146

<151> 2000-07-02

<160> 43

<170> PatentIn version 3.2 (1-26) and 3.4 (27-43)

<210> 1

<211> 1650

<212> DNA

<213> Bacillus pumilus

<220>

<221> CDS

<222> (1)..(1650)

<400> 1

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1 5 10 15	

tat tac acc cct aaa gtt att gct gac ttt tta tgt caa tgg agt att	96
Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile	
20 25 30	

caa gat gac aca aag agt gta ctt gaa ccc agt tgt gga gat ggt aat	144
Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn	
35 40 45	

ttt att gaa tcg gca ata ctt agg ttc aaa gaa ctt agt ata gat aat	192
Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn	
50 55 60	

gaa caa ctt aaa gga aga att aca gga gta gag cta att gaa gaa gaa	240
Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu	
65 70 75 80	

gct ttg aaa gtt caa aat cga gca aat gag ttg ggg gtt gat aaa aac	288
Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn	

85

90

95

tca ata gta aat agt gac ttc ttt caa ttt gta aaa gat aat aag aat 336
 Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn
 100 105 110

aaa aaa ttt gat act att att ggt aat cca cca ttc ata aga tac caa 384
 Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln
 115 120 125

aac ttt cct gaa gag cat cgt agt ata gcc atg gaa atg atg gag gaa 432
 Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu
 130 135 140

cta ggt tta aaa cct aat aaa ctt aca aat atc tgg gtt cca ttt cta 480
 Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu
 145 150 155 160

gtg gta tct gct aca tta ctt aat gaa caa gga aag atg gct atg gtt 528
 Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val
 165 170 175

ata ccg gct gaa tta ttt cag gta aag tat gca gca gaa aca aga att 576
 Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile
 180 185 190

ttt tta tca aag ttt ttc gat cgt atc act ata att aca ttt gaa aaa 624
 Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys
 195 200 205

ctt gtt ttt gaa aat atc caa cag gaa gtt ata cta ctt ctt tgt gaa 672
 Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu
 210 215 220

aag aaa gtt aat aaa ggt aaa gga att cgg gtt att gaa tgc gag aac 720
 Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn
 225 230 235 240

tta gat gga tta aat tcc att gat ttt gta gct ata aat ggt tca aat 768
 Leu Asp Gly Leu Asn Ser Ile Asp Phe Val Ala Ile Asn Gly Ser Asn
 245 250 255

gtt aaa cct att gaa cac cgt act gaa aag tgg aca aag tat ttc tta 816
 Val Lys Pro Ile Glu His Arg Thr Glu Lys Trp Thr Lys Tyr Phe Leu
 260 265 270

aac gaa gat gaa ata ctt ctt tta cag agt tta aag gaa gac aaa cgc 864
 Asn Glu Asp Glu Ile Leu Leu Leu Gln Ser Leu Lys Glu Asp Lys Arg
 275 280 285

gtt aaa aat tgt aat gac tat ttt aag aca gaa gtt ggc tta gtt act 912
 Val Lys Asn Cys Asn Asp Tyr Phe Lys Thr Glu Val Gly Leu Val Thr
 290 295 300

gga cga aac gaa ttc ttt atg atg aaa gaa aac caa gta aaa gaa tgg 960
 Gly Arg Asn Glu Phe Phe Met Met Lys Glu Asn Gln Val Lys Glu Trp

305	310	315	320	
aat cta gaa gaa tat aca ata cct gtt aca ggt agg tcc aat cag tta Asn Leu Glu Glu Tyr Thr Ile Pro Val Thr Gly Arg Ser Asn Gln Leu				1008
	325	330	335	
aaa ggt ata aca ttt aca gaa aat gat ttt cat gaa aat tca atg gaa Lys Gly Ile Thr Phe Thr Glu Asn Asp Phe His Glu Asn Ser Met Glu				1056
	340	345	350	
caa aag gca att cac cta ttt ttg cca cca gat gaa gat ttt gaa aag Gln Lys Ala Ile His Leu Phe Leu Pro Pro Asp Glu Asp Phe Glu Lys				1104
	355	360	365	
tta ccg att gag tgt caa aat tat atc aag tat ggg gaa gaa aaa ggc Leu Pro Ile Glu Cys Gln Asn Tyr Ile Lys Tyr Gly Glu Glu Lys Gly				1152
	370	375	380	
ttc cat caa ggc tat aaa acc aga att aga aaa cgt tgg tat ata act Phe His Gln Gly Tyr Lys Thr Arg Ile Arg Lys Arg Trp Tyr Ile Thr				1200
	385	390	395	400
cca tct aga tgg gtt cca gat gct ttt gct tta aga cag gtt gat ggc Pro Ser Arg Trp Val Pro Asp Ala Phe Ala Leu Arg Gln Val Asp Gly				1248
	405	410	415	
tat cca aaa cta att tta aat gaa acc gac gct tct tct act gat aca Tyr Pro Lys Leu Ile Leu Asn Glu Thr Asp Ala Ser Ser Thr Asp Thr				1296
	420	425	430	
att cat agg gtt aga ttt aaa gaa ggt ata aat gaa aag tta gcc gta Ile His Arg Val Arg Phe Lys Glu Gly Ile Asn Glu Lys Leu Ala Val				1344
	435	440	445	
gtt tca ttt ttg aac tca ctc act ttt gca tct tca gaa ata acg ggg Val Ser Phe Leu Asn Ser Leu Thr Phe Ala Ser Ser Glu Ile Thr Gly				1392
	450	455	460	
aga agt tat ggt ggt ggt gtt atg aca ttc gaa cca act gaa att gga Arg Ser Tyr Gly Gly Gly Val Met Thr Phe Glu Pro Thr Glu Ile Gly				1440
	465	470	475	480
gaa atc cta ata cct tcc ttt gat aac tta tcc att gat ttt gat aaa Glu Ile Leu Ile Pro Ser Phe Asp Asn Leu Ser Ile Asp Phe Asp Lys				1488
	485	490	495	
att gat gcc tta att cga gaa aag gag att gaa aaa gtc ctt gat att Ile Asp Ala Leu Ile Arg Glu Lys Glu Ile Glu Lys Val Leu Asp Ile				1536
	500	505	510	
gtt gat gaa gct tta ctt ata aaa tat cat ggg ttt agt gag aaa gaa Val Asp Glu Ala Leu Leu Ile Lys Tyr His Gly Phe Ser Glu Lys Glu				1584
	515	520	525	
gta aaa cag ctt cga ggg ata tgg aag aaa ctt tct cag aga aga aac Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn				1632

530

535

540

aat aga acg aag aaa taa

1650

Asn Arg Thr Lys Lys

545 550

<210> 2

<211> 549

<212> PRT

<213> Bacillus pumilus

<400> 2

Met Asn Gln Leu Ile Glu Asn Val Asn Leu Gln Lys Leu Arg Gly Gly

1 5 10 15

Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile

20 25 30

Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn

35 40 45

Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn

50 55 60

Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu

65 70 75 80

Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn

85 90 95

Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn

100 105 110

Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln

115 120 125

Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu

130 135 140

Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu

145 150 155 160

Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val

165 170 175

Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile

180 185 190

Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys

195 200 205

Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu

210 215 220

Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn

225		230		235		240
Leu Asp Gly	Leu Asn Ser Ile Asp Phe Val Ala Ile Asn Gly Ser Asn					
	245		250		255	
Val Lys Pro	Ile Glu His Arg Thr Glu Lys Trp Thr Lys Tyr Phe Leu					
	260		265		270	
Asn Glu Asp	Glu Ile Leu Leu Leu Gln Ser Leu Lys Glu Asp Lys Arg					
	275		280		285	
Val Lys Asn	Cys Asn Asp Tyr Phe Lys Thr Glu Val Gly Leu Val Thr					
	290		295		300	
Gly Arg Asn	Glu Phe Phe Met Met Lys Glu Asn Gln Val Lys Glu Trp					
305		310		315		320
Asn Leu Glu	Glu Tyr Thr Ile Pro Val Thr Gly Arg Ser Asn Gln Leu					
	325		330		335	
Lys Gly Ile	Thr Phe Thr Glu Asn Asp Phe His Glu Asn Ser Met Glu					
	340		345		350	
Gln Lys Ala	Ile His Leu Phe Leu Pro Pro Asp Glu Asp Phe Glu Lys					
	355		360		365	
Leu Pro Ile	Glu Cys Gln Asn Tyr Ile Lys Tyr Gly Glu Glu Lys Gly					
	370		375		380	
Phe His Gln	Gly Tyr Lys Thr Arg Ile Arg Lys Arg Trp Tyr Ile Thr					
385		390		395		400
Pro Ser Arg	Trp Val Pro Asp Ala Phe Ala Leu Arg Gln Val Asp Gly					
	405		410		415	
Tyr Pro Lys	Leu Ile Leu Asn Glu Thr Asp Ala Ser Ser Thr Asp Thr					
	420		425		430	
Ile His Arg	Val Arg Phe Lys Glu Gly Ile Asn Glu Lys Leu Ala Val					
	435		440		445	
Val Ser Phe	Leu Asn Ser Leu Thr Phe Ala Ser Ser Glu Ile Thr Gly					
	450		455		460	
Arg Ser Tyr	Gly Gly Gly Val Met Thr Phe Glu Pro Thr Glu Ile Gly					
465		470		475		480
Glu Ile Leu	Ile Pro Ser Phe Asp Asn Leu Ser Ile Asp Phe Asp Lys					
	485		490		495	
Ile Asp Ala	Leu Ile Arg Glu Lys Glu Ile Glu Lys Val Leu Asp Ile					
	500		505		510	
Val Asp Glu	Ala Leu Leu Ile Lys Tyr His Gly Phe Ser Glu Lys Glu					
	515		520		525	

Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn
530 535 540

Asn Arg Thr Lys Lys
545

<210> 3

<211> 3030

<212> DNA

<213> Bacillus pumilus

<220>

<221> CDS

<222> (1)..(3030)

<400> 3

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1 5 10 15

ttt tta aaa cca act tat aat gaa act caa cta agg aat gat ttt ata 96
Phe Leu Lys Pro Thr Tyr Asn Glu Thr Gln Leu Arg Asn Asp Phe Ile
20 25 30

gac cca ctt cta aaa tct tta gga tgg gat gtt gat aat acc aaa gga 144
Asp Pro Leu Leu Lys Ser Leu Gly Trp Asp Val Asp Asn Thr Lys Gly
35 40 45

aaa aca cat att cta aga gat gtc att caa gaa gaa tac ata gaa ata 192
Lys Thr His Ile Leu Arg Asp Val Ile Gln Glu Glu Tyr Ile Glu Ile
50 55 60

aaa gat gag gag aca aag aaa aat cca gat tat aca ctt cgt ata aac 240
Lys Asp Glu Glu Thr Lys Lys Asn Pro Asp Tyr Thr Leu Arg Ile Asn
65 70 75 80

ggg acg aga aag ctg ttt gta gag gtt aag aaa ccg tct ttt aat att 288
Gly Thr Arg Lys Leu Phe Val Glu Val Lys Lys Pro Ser Phe Asn Ile
85 90 95

ttg aaa tca gct aaa gca gcc ttc caa aca aga aga tat ggt tgg agt 336
Leu Lys Ser Ala Lys Ala Ala Phe Gln Thr Arg Arg Tyr Gly Trp Ser
100 105 110

gct aac ctt ggt att tca gta ctt aca aat ttc gag cat cta gtt att 384
Ala Asn Leu Gly Ile Ser Val Leu Thr Asn Phe Glu His Leu Val Ile
115 120 125

tat gat tgt aga tat acg cct gac aaa tcc gac aat gaa cat att gct 432
Tyr Asp Cys Arg Tyr Thr Pro Asp Lys Ser Asp Asn Glu His Ile Ala
130 135 140

aga tat aaa gtt ttc tct tac gag gaa tat gaa gaa gca ttt gat gaa 480

Arg	Tyr	Lys	Val	Phe	Ser	Tyr	Glu	Glu	Tyr	Glu	Glu	Ala	Phe	Asp	Glu	
145					150					155					160	
ata	aag	gat	ata	att	tca	tat	gag	tca	gcc	aac	tca	ggg	gct	ctg	gac	528
Ile	Lys	Asp	Ile	Ile	Ser	Tyr	Glu	Ser	Ala	Asn	Ser	Gly	Ala	Leu	Asp	
				165					170					175		
gaa	atg	ttt	gat	gta	aat	aca	aga	gtt	ggg	gaa	acg	ttt	gac	gag	tat	576
Glu	Met	Phe	Asp	Val	Asn	Thr	Arg	Val	Gly	Glu	Thr	Phe	Asp	Glu	Tyr	
			180					185					190			
ttt	tta	cag	caa	att	gag	aat	tgg	cgc	gaa	aag	cta	gct	aaa	act	gca	624
Phe	Leu	Gln	Gln	Ile	Glu	Asn	Trp	Arg	Glu	Lys	Leu	Ala	Lys	Thr	Ala	
		195					200					205				
att	aaa	aat	aac	acc	gaa	tta	ggg	gaa	gag	gac	gtc	aat	ttt	att	gtc	672
Ile	Lys	Asn	Asn	Thr	Glu	Leu	Gly	Glu	Glu	Asp	Val	Asn	Phe	Ile	Val	
	210					215				220						
caa	aga	cta	tta	aac	aga	att	att	ttt	ctt	aga	gtt	tgt	gaa	gat	aga	720
Gln	Arg	Leu	Leu	Asn	Arg	Ile	Ile	Phe	Leu	Arg	Val	Cys	Glu	Asp	Arg	
225					230					235					240	
acc	att	gaa	aaa	tat	gaa	aca	att	aaa	agt	ata	aaa	aac	tat	gag	gaa	768
Thr	Ile	Glu	Lys	Tyr	Glu	Thr	Ile	Lys	Ser	Ile	Lys	Asn	Tyr	Glu	Glu	
				245					250					255		
tta	aaa	gat	ctg	ttt	caa	aag	tct	gat	agg	aaa	ttt	aat	tca	ggg	ctc	816
Leu	Lys	Asp	Leu	Phe	Gln	Lys	Ser	Asp	Arg	Lys	Phe	Asn	Ser	Gly	Leu	
			260					265					270			
ttt	gac	ttc	ata	gat	gat	acg	ctc	ttg	ctt	gag	gtt	gaa	att	gat	tcg	864
Phe	Asp	Phe	Ile	Asp	Asp	Thr	Leu	Leu	Leu	Glu	Val	Glu	Ile	Asp	Ser	
	275						280					285				
aat	gta	ttg	ata	gaa	att	ttt	agt	gat	tta	tat	ttc	cca	caa	agc	cca	912
Asn	Val	Leu	Ile	Glu	Ile	Phe	Ser	Asp	Leu	Tyr	Phe	Pro	Gln	Ser	Pro	
	290					295					300					
tat	gat	ttt	tct	gtt	gtc	gat	cca	aca	ata	tta	agc	cag	ata	tat	gaa	960
Tyr	Asp	Phe	Ser	Val	Val	Asp	Pro	Thr	Ile	Leu	Ser	Gln	Ile	Tyr	Glu	
305					310					315					320	
cgt	ttt	cta	ggg	caa	gaa	ata	att	ata	gag	tca	ggg	ggg	aca	ttt	cac	1008
Arg	Phe	Leu	Gly	Gln	Glu	Ile	Ile	Ile	Glu	Ser	Gly	Gly	Thr	Phe	His	
				325					330					335		
att	acg	gag	tca	cca	gaa	gtt	gcg	gcg	tcc	aat	ggg	gtt	gtt	cca	act	1056
Ile	Thr	Glu	Ser	Pro	Glu	Val	Ala	Ala	Ser	Asn	Gly	Val	Val	Pro	Thr	
			340					345					350			
cca	aaa	att	atc	gtc	gaa	cag	ata	gtg	aaa	gac	act	tta	acg	ccc	ctt	1104
Pro	Lys	Ile	Ile	Val	Glu	Gln	Ile	Val	Lys	Asp	Thr	Leu	Thr	Pro</		

370

375

380

ata tgt tgt gga tca gga act ttc cta att tca agt tat gac ttt cta 1200
Ile Cys Cys Gly Ser Gly Thr Phe Leu Ile Ser Ser Tyr Asp Phe Leu
385 390 395 400

gta gag aaa gta atg gaa aag ata ata gaa gag aac atc gat gat tca 12